

PCV18

FACTORS ASSOCIATED WITH RISK OF METABOLIC SYNDROME FOR US FIRST GENERATION ADOLESCENTS (AGES 12-17)

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OBJECTIVE: To contrast the factors that are associated with metabolic syndrome risk for first generation adolescents and US non-immigrant adolescents. **METHODS:** At risk is defined as having one or more of the following: elevated fasting glucose, elevated SBP, elevated BMI, 75th percentile waist circumference, or low HDL. Logistic regression and NHANES 2005-2006 data were used to examine the impact on metabolic syndrome risks; gender, ethnicity, length of residence, income, and number of meals eaten outside the home per week. First generation Hispanic and non-Hispanic adolescents are compared with adolescent non-immigrants. A significance level of 0.05 was used. Sample sizes for Hispanic first generation adolescents, non-Hispanic first generation adolescents, and non-immigrant adolescents are 1,076,059, 674,536, and 22,091,170 respectively. **RESULTS:** About 71% of first generation adolescent Hispanics, 67% for non-Hispanic other first generation adolescents, and 67% of non-immigrant adolescents are at risk for metabolic syndrome. Significant predictors for risk among Hispanics are female gender, longer time of residence in the United States, and low familial income. For every one meal eaten outside the home risk increases by 11%. For other non-Hispanics, the male gender is a negative predictor along with low and middle familial income levels. Length of residence in the United States and meals eaten outside the home were not significant predictors. Among the non-immigrants, male gender is a negative predictor, while low and middle income increase risk by 60% and 47% respectively. Each meal eaten outside the home increases their risk by 3%. **CONCLUSION:** These adolescents are at risk for acute cardiovascular endpoints, higher medical utilization and expenditure, and lower quality of life. Interventions should focus on education regarding healthy eating outside the home with limited resources. A surprising result of this analysis is the high price of acculturation for Hispanic first generation adolescents in particular.

PCV19

RESIDUAL DYSLIPIDEMIA ON SIMVASTATIN: POPULATION MODELING OF OPTIMAL LIPID VALUE ACHIEVEMENT WITH ADDED EXTENDED-RELEASE NIACIN VERSUS EZETIMIBEStanek E¹, Charland S²¹None, Thorofare, NJ, USA, ²School of Pharmacy, University of Colorado, Winter Park, CO, USA

OBJECTIVE: To compare the population modeling effects of simvastatin alone, simvastatin plus ezetimibe and simvastatin plus extended-release niacin (ERN) on achievement of individual and combined optimal lipid values in untreated managed care patients with coronary heart disease (CHD) or risk equivalent (CHD/RE). **METHODS:** Patients with a baseline lipid panel between January 1, 2000-December 31, 2001, no concomitant dyslipidemia therapy, continuous eligibility for 24 months, and CHD or CHD/RE by diagnosis or procedure were analyzed from a 2.1 million record managed care database (HealthCore, Inc. Research Integrated Dataset). Patient-level lipids were assessed for achievement of guideline-defined optimal lipid values for LDL-C (<100 mg/dL), HDL-C (>40 mg/dL men; >50 mg/dL women), triglycerides (TG; <150 mg/dL), non-HDL-C (<130 mg/dL), and combined LDL-C + HDL-C + TG at untreated baseline, after simvastatin 40 mg, after simvastatin + ezetimibe 10 mg, and after simvastatin + ERN 1 g and 2 g. Treatment effects were modeled based on product labeling, assuming additivity for sim-

vastatin and ERN. Primary outcome measure was percentage of patients with nonoptimal values. **RESULTS:** Analysis included 20,948 patients: 49% female, mean (\pm SD) age 65 ± 14 years, hypertension 62%, diabetes 34%. At untreated baseline, nonoptimal values occurred in 79% for LDL-C, 43% HDL-C, 42% TG, 77% nonHDL-C, and 92% for combined lipids. After modeled therapy, nonoptimal value frequencies were: simvastatin LDL-C 34%, HDL-C 14%, TG 34%, nonHDL-C 36%, and combined 69% ($p < 0.05$ vs baseline); simvastatin + ezetimibe LDL-C 21%, HDL-C 23%, TG 32%, nonHDL-C 31%, and combined 53% ($p < 0.05$ vs baseline, simvastatin); simvastatin + ERN 1 g and 2 g LDL-C 25% and 18%, HDL-C 0.2% and 0%, TG 30% and 22%, nonHDL-C 20% and 10%, and combined 46% and 36% [$p < 0.05$ vs baseline, simvastatin, simvastatin + ezetimibe ($p = \text{NS}$ for TG at 1 g dose)]. **CONCLUSION:** In this high-risk population, nonoptimal lipid values were very prevalent and persisted after modeled simvastatin 40 mg. Modeled simvastatin + ERN 1-2 g diminished residual dyslipidemia and nonoptimal lipid values more than simvastatin + ezetimibe.

PCV20

UPDATING THE RXRISK-V: CREATING A CROSSWALK BETWEEN VA AND FIRSTDATABANK THERAPEUTIC CATEGORIES

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OBJECTIVE: Co-morbidity indices based on drug utilization have been used to predict costs of care. The original RxRisk co-morbid disease index was based on United States (US) National Drug Code (NDC) numbers, and as such, needed to be updated at the NDC level for any change in manufacturer, repackager, or generic status, or with the introduction of each new molecular entity to the US market. The RxRisk-V was a modification of the original that used Veteran Affairs (VA) drug codes rather than NDC numbers to assign co-morbidity status for a set of diseases. Use of VA drug codes rather than NDCs simplifies the process of updating the tool. We undertook to create a crosswalk between VA drug codes and FirstDataBank (FDB) categories so the tool could be used with non-VA pharmacy data. **METHODS:** We obtained SAS code and disease category tables for the RxRisk-V. Clinical pharmacists reviewed the RxRisk-V disease categories and created an algorithm for mapping VA therapeutic categories to FDB specific drug therapeutic class categories. Pharmacists also updated disease categories to include drugs that would not have been updated in the RxRisk-V due to new therapeutic categories introduced since 1999. Generic name, brand name, and route of administration fields were used to specify which agents within each FDB therapeutic class were predictive of each RxRisk-V disease category. The SAS code for the RxRisk-V was modified to crosswalk between VA codes and non-VA pharmacy data. **RESULTS:** We successfully applied the crosswalk to a cohort of 19,458 patients from the RxAmerica database and generated co-morbidity scores. **CONCLUSION:** Using the RxRisk-V enables investigators to apply an updated co-morbid disease severity index to VA pharmacy data. We created a crosswalk to enable use with non-VA pharmacy data. Future work is needed to validate the tool with the crosswalk incorporated.